

#8



1600

RAW SEQUENCE LISTING

DATE: 06/05/2002

PATENT APPLICATION: US/09/641,701A

TIME: 14:57:29

Input Set : A:\195870US0.txt

Output Set: N:\CRF3\06052002\I641701A.raw

3 <110> APPLICANT: KOJIMA, Yoshinao
 4 FUKUMOTO, Satoshi
 5 FURUKAWA, Keiko
 6 OKAJIMA, Tetsuya
 7 FURUKAWA, Koichi
 9 <120> TITLE OF INVENTION: ALPHA 1,4-GALACTOSYLTRANSFERASE AND DNA ENCODING THEREOF
 11 <130> FILE REFERENCE: 195870US0
 13 <140> CURRENT APPLICATION NUMBER: 09/641,701A
 14 <141> CURRENT FILING DATE: 2000-08-21
 16 <150> PRIOR APPLICATION NUMBER: JP 2000-35454
 17 <151> PRIOR FILING DATE: 2000-02-14
 19 <160> NUMBER OF SEQ ID NOS: 2
 21 <170> SOFTWARE: PatentIn version 3.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1975
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (134)..(1192)
 31 <223> OTHER INFORMATION:
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 37 cctctctgca atgggctgcc caggctgacc agccgggtcc tgctggaagc tcctgggtctg 120
 39 atctggggat acc atg tcc aag ccc ccc gac ctg ctg cgg ctg ctg 169
 40 Met Ser Lys Pro Pro Asp Leu Leu Arg Leu Leu
 41 1 5 10
 43 cgg ggc gcc cca agg cag cgg gtc tgc acc ctg ttc atc atc ggc ttc 217
 44 Arg Gly Ala Pro Arg Gln Arg Val Cys Thr Leu Phe Ile Ile Gly Phe
 45 15 20 25
 47 aag ttc acg ttt ttc gtc tcc atc atg atc tac tgg cac gtt gtg gga 265
 48 Lys Phe Thr Phe Phe Val Ser Ile Met Ile Tyr Trp His Val Val Gly
 49 30 35 40
 51 gag ccc aag gag aaa ggg cag ctg tat aac ctg cca gca gag atc ccc 313
 52 Glu Pro Lys Glu Lys Gly Gln Leu Tyr Asn Leu Pro Ala Glu Ile Pro
 53 45 50 55 60
 55 tgc ccc acc ttg aca ccc ccc acc cca ccc tcc cac ggc ccc act cca 361
 56 Cys Pro Thr Leu Thr Pro Pro Thr Pro Pro Ser His Gly Pro Thr Pro
 57 65 70 75
 59 ggc aac atc ttc ttc ctg gag act tca gac cgg acc aac ccc aac ttc 409
 60 Gly Asn Ile Phe Phe Leu Glu Thr Ser Asp Arg Thr Asn Pro Asn Phe
 61 80 85 90
 63 ctg ttc atg tgc tcg gtg gag tcg gcc gcc aga act cac ccc gaa tcc 457

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64 Leu Phe Met Cys Ser Val Glu Ser Ala Ala Arg Thr His Pro Glu Ser
65          95          100          105
67 cac gtg ctg gtc ctg atg aaa ggg ctt ccg ggt ggc aac gcc tct ctg      505
68 His Val Leu Val Leu Met Lys Gly Leu Pro Gly Gly Asn Ala Ser Leu
69      110          115          120
71 ccc cgg cac ctg ggc atc tca ctt ctg agc tgc ttc ccg aat gtc cag      553
72 Pro Arg His Leu Gly Ile Ser Leu Leu Ser Cys Phe Pro Asn Val Gln
73 125          130          135          140
75 atg ctc ccg ctg gac ctg cgg gag ctg ttc cgg gac aca ccc ctg gcc      601
76 Met Leu Pro Leu Asp Leu Arg Glu Leu Phe Arg Asp Thr Pro Leu Ala
77          145          150          155
79 gac tgg tac gcg gcc gtg cag ggg cgc tgg gag ccc tac ctg ctg ccc      649
80 Asp Trp Tyr Ala Ala Val Gln Gly Arg Trp Glu Pro Tyr Leu Leu Pro
81          160          165          170
83 gtg ctc tcc gac gcc tcc agg atc gca ctc atg tgg aag ttc ggc ggc      697
84 Val Leu Ser Asp Ala Ser Arg Ile Ala Leu Met Trp Lys Phe Gly Gly
85      175          180          185
87 atc tac ctg gac acg gac ttc att gtt ctc aag aac ctg cgg aac ctg      745
88 Ile Tyr Leu Asp Thr Asp Phe Ile Val Leu Lys Asn Leu Arg Asn Leu
89      190          195          200
91 acc aac gtg ctg ggc acc cag tcc cgc tac gtc ctc aac ggc gcg ttc      793
92 Thr Asn Val Leu Gly Thr Gln Ser Arg Tyr Val Leu Asn Gly Ala Phe
93 205          210          215          220
95 ctg gcc ttc gag cgc cgg cac gag ttc atg gcg ctg tgc atg cgg gac      841
96 Leu Ala Phe Glu Arg Arg His Glu Phe Met Ala Leu Cys Met Arg Asp
97          225          230          235
99 ttc gtg gac cac tac aac ggc tgg atc tgg ggt cac cag ggc ccg cag      889
100 Phe Val Asp His Tyr Asn Gly Trp Ile Trp Gly His Gln Gly Pro Gln
101          240          245          250
103 ctg ctc acg cgg gtc ttc aag aag tgg tgt tcc atc cgc agc ctg gcc      937
104 Leu Leu Thr Arg Val Phe Lys Lys Trp Cys Ser Ile Arg Ser Leu Ala
105          255          260          265
107 gag agc cgc gcc tgc cgc ggc gtc acc acc ctg ccc cct gag gcc ttc      985
108 Glu Ser Arg Ala Cys Arg Gly Val Thr Thr Leu Pro Pro Glu Ala Phe
109      270          275          280
111 tac ccc atc ccc tgg cag gac tgg aag aag tac ttt gag gac atc aac      1033
112 Tyr Pro Ile Pro Trp Gln Asp Trp Lys Lys Tyr Phe Glu Asp Ile Asn
113 285          290          295          300
115 ccg gag gag ctg ccg cgg ctg ctc agt gcc acc tat gct gtc cac gtg      1081
116 Pro Glu Glu Leu Pro Arg Leu Leu Ser Ala Thr Tyr Ala Val His Val
117          305          310          315
119 tgg aac aag aag agc cag ggc acg cgg ttc gag gcc acg tcc agg gca      1129
120 Trp Asn Lys Lys Ser Gln Gly Thr Arg Phe Glu Ala Thr Ser Arg Ala
121          320          325          330
123 ctg ctg gcc cag ctg cat gcc cgc tac tgc ccc acg acg cac gag gcc      1177
124 Leu Leu Ala Gln Leu His Ala Arg Tyr Cys Pro Thr Thr His Glu Ala
125          335          340          345
127 atg aaa atg tac ttg tgaggggccc gccaggtcac ctccccaacc tgctcctgat      1232
128 Met Lys Met Tyr Leu

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129      350
131 ggggcactgg gccgcccttc cccggggaggg aagattgagg gcccgggaga gggaggcccg 1292
133 agctgccacc gggcttaggc aggctgttga ggagctgtgg gagcaggccc agtgggaggg 1352
135 tgtggacacc ccgaggacag tgtcctgtct cgaggcaggg ctgacacatg gtgccatagc 1412
137 cagcggaggg cgctcagtga gtgccccggg ccttctagac aacaggcagg aaggatgaac 1472
139 ctgagggcac ccccagggtg tgcggaaagc caggcagttg ggacagaggt gccacagagg 1532
141 gcagaggccg gtgctaaggg gatggggaag aagggacaag attcccagag aggagaggag 1592
143 gctgttggtg ggaaagtggc agggctgggg gagaccagc cccaagggtc cggggcggag 1652
145 gatgctttgt tcttttctgg ttttggttcc tctttcgcgg ggggtggggg aggtcaacag 1712
147 ggactgagtg gggcagaggg ccagaagtgc cagcctgggg agccgtttgg gggcagcccc 1772
149 ttctgcccac cccatccttc ttcctctcca gagatgccag gggggcgtgt atgctctgcc 1832
151 ccttccctca gacaggggct ggggtggggg gctctttagg ctgaggagaa gcattttaaa 1892
153 gaaaccccca cctgcccgc cgcattataa acacaggaga ataatcaata gaataaaagt 1952
155 gaccgactgt caaaaaaaaa aaa 1975
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159 <211> LENGTH: 353
160 <212> TYPE: PRT
161 <213> ORGANISM: Homo sapiens
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170 20 25 30
173 Phe Val Ser Ile Met Ile Tyr Trp His Val Val Gly Glu Pro Lys Glu
174 35 40 45
177 Lys Gly Gln Leu Tyr Asn Leu Pro Ala Glu Ile Pro Cys Pro Thr Leu
178 50 55 60
181 Thr Pro Pro Thr Pro Pro Ser His Gly Pro Thr Pro Gly Asn Ile Phe
182 65 70 75 80
185 Phe Leu Glu Thr Ser Asp Arg Thr Asn Pro Asn Phe Leu Phe Met Cys
186 85 90 95
189 Ser Val Glu Ser Ala Ala Arg Thr His Pro Glu Ser His Val Leu Val
190 100 105 110
193 Leu Met Lys Gly Leu Pro Gly Gly Asn Ala Ser Leu Pro Arg His Leu
194 115 120 125
197 Gly Ile Ser Leu Leu Ser Cys Phe Pro Asn Val Gln Met Leu Pro Leu
198 130 135 140
201 Asp Leu Arg Glu Leu Phe Arg Asp Thr Pro Leu Ala Asp Trp Tyr Ala
202 145 150 155 160
205 Ala Val Gln Gly Arg Trp Glu Pro Tyr Leu Leu Pro Val Leu Ser Asp
206 165 170 175
209 Ala Ser Arg Ile Ala Leu Met Trp Lys Phe Gly Gly Ile Tyr Leu Asp
210 180 185 190
213 Thr Asp Phe Ile Val Leu Lys Asn Leu Arg Asn Leu Thr Asn Val Leu
214 195 200 205
217 Gly Thr Gln Ser Arg Tyr Val Leu Asn Gly Ala Phe Leu Ala Phe Glu
218 210 215 220
221 Arg Arg His Glu Phe Met Ala Leu Cys Met Arg Asp Phe Val Asp His
222 225 230 235 240

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225 Tyr Asn Gly Trp Ile Trp Gly His Gln Gly Pro Gln Leu Leu Thr Arg
226                245                250                255
229 Val Phe Lys Lys Trp Cys Ser Ile Arg Ser Leu Ala Glu Ser Arg Ala
230                260                265                270
233 Cys Arg Gly Val Thr Thr Leu Pro Pro Glu Ala Phe Tyr Pro Ile Pro
234                275                280                285
237 Trp Gln Asp Trp Lys Lys Tyr Phe Glu Asp Ile Asn Pro Glu Glu Leu
238                290                295                300
241 Pro Arg Leu Leu Ser Ala Thr Tyr Ala Val His Val Trp Asn Lys Lys
242 305                310                315                320
245 Ser Gln Gly Thr Arg Phe Glu Ala Thr Ser Arg Ala Leu Leu Ala Gln
246                325                330                335
249 Leu His Ala Arg Tyr Cys Pro Thr Thr His Glu Ala Met Lys Met Tyr
250                340                345                350
253 Leu

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VERIFICATION SUMMARY

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